



Example 4

## Mapping of Nucleic Acid Sequences on the Human Genome

Human genes were mapped using the Stanford G3 Hybrid Panel (Stewart et al., 1997), which is marketed by Research Genetics, Huntsville, Alabama. This panel consists of 83 different genomic DNAs of human-hamster hybrid cell lines and allows resolution of 500 kilobases. The hybrid cell lines were obtained by fusion of irradiated diploid human cells with cells of the Chinese hamster. The retention pattern of the human chromosome fragments is determined by means of gene-specific primers in a polymerase chain reaction and is analyzed using software available from the Stanford RH server ([http://www.stanford.edu/RH/rhserver\\_form2.html](http://www.stanford.edu/RH/rhserver_form2.html)). This program determines the STS marker that is nearest to the desired gene. The corresponding cytogenetic band was determined using the "Mapview" program of the Genome Database (GDB), (<http://gdbwww.dkfz-heidelberg.de>).

In addition to mapping of genes on the human chromosome set by various experimental methods, it is possible to determine the location of genes on this by biocomputer methods. To do this, the known program e-PCR was used (Schuler GD (1998) Electronic PCR: Bridging the Gap between Genome Mapping and Genome Sequencing. Trends Biotechnol 16: 456-459, Schuler GD (1997). Sequence Mapping by Electronic PCR. Genome Res. 7: 541-550). The database used here no longer corresponds to the one cited in the literature, but is a further development which includes data from the public database RHdb (<http://www.ebi.ac.uk/RHdb/index.html>). Analogously to the mapping by the hybrid panels,

the results were evaluated with the above-mentioned software and  
the software of the Whitehead Institute  
(<http://carbon.wi.mit.edu:8000/cgi-bin/contig/rhmapper.pl>).

**TABLE I**

Col. 1 - Sequence ID No.:

Col. 2 - Expression in hysteromyomic tissue:

Col. 3 - Function

Col. 4 - Modules

Col. 5 - Length of the applied sequence in bases

Col. 6 - Cytogenetic localization

Col. 7 - Next marker

[Key to Table I:]

[Col. 2:] erhöht = elevated

[Col. 3:]

[Seq. ID No.: 14, 15, 17, 30, 31] unbekannt = unknown

[Seq. ID No.: 16] Homolog zu Homo sapiens... = homologous  
to homo sapiens...

[Seq. ID No.: 18] Humanes Homolog zu ... = human homolog to

[Seq. ID No.: 52] Verlängerung von Seq. ID. 14 =  
Lengthening of Seq. ID. 14

TABELLE I

TABLE I

Sequenz ID No.:	Expression im Uterus-Myomgewebe:	Funktion	Module	Länge der angenommenen Sequenz in Basen	Cylogenetische Lokalisation	nächster Marker
1	erhöht	Human mRNA for ornithine decarboxylase antizyme Human MEST mRNA	"abhydro-lase"	2310	779	D5S1730
2	erhöht	Human cocaine and amphetamine regulated transcript		854	5q11.2-q13.1	
3	erhöht	CART (hCART)		1112	1p36.11-p36.13	D2S387
4	erhöht	Human nicotinib-associated glycoprotein (MFAP2)		1051	2p23.3	
5	erhöht	Human mRNA for KIAA0108 gene	"kazal"	1516	5q32-q33.1	
6	erhöht	Human SPARC/closteoneoclin	"rrn"	2367	2p22.3-p22.1	WT-9798
7	erhöht	Human <i>sapiens</i> splicing factor, arginine/serine-rich 7 (SFRS7)		568		
8	erhöht	Human diisopropylate isomerase	3x "TIM"	1775		
9	erhöht	Human nuclear ribonucleoprotein particle (hnRNP) C	"Thymosin"	509		
10	erhöht	Human thyinosin beta-4	"GFBP"	2191	7p12.2-p13	
11	erhöht	Human growth hormone-dependent insulin-like growth factor-binding protein mRNA	"hydra-globulin 1"			
12	erhöht	Human H19	"Ipcocain"	1769		
13	erhöht	Human cellular retinoic acid binding protein II (CRABP)	"rrn"	1026		
14	erhöht	unbekannt		676	14p11.2-14p11.1	WT-4204
15	erhöht	unbekannt		1254		
16	erhöht	Homolog zu <i>Homo sapiens</i> mRNA (or putatively prenylated protein)		537		
17	erhöht	Humanes Homolog zu P. vivax <i>lwal</i> gene		823		
18	erhöht	Human tunican mRNA	5x "LRR"	1082		
19	erhöht	Human 37 kD laminin receptor precursor/p40 ribosome associated protein	"S2"	1540	12q21.31-12q21.33	D12S351
20	erhöht	Human YMP	"PMP22"	844		
21	erhöht	Human NADH:ubiquinone oxidoreductase M1/M2Q subunit	"G-alpha", "ar"	862		
22	erhöht	Human mRNA for coupling protein G(s) alpha-subunit	"rrn"	546		
23	erhöht	Human mRNA for non-histone chromosomal protein		1591	20q13.32-q13.33	
24	erhöht	Human hnRNP core protein A1	"HMG14_17"	441		
25	erhöht	Human hnRNP core protein A1		1131		
26	erhöht	<i>H. sapiens</i> mRNA for prolactin (clone PR1.205)	"laminone"	1071		
27	erhöht	Human mRNA for neurile growth-promoting protein.	3x "PTN_MK"	896		
28	erhöht	<i>H. sapiens</i> mRNA for proliferation-associated gene (pag)	"AhpC-TSA"	1050	1p32.3-p34.3	
29	erhöht	<i>H. sapiens</i> alpha NAC		581		
30	erhöht	unbekannt		264		
31	erhöht	unbekannt		111		
52	erhöht	Verlängerung von Seq. ID. 14	"rrn"	3665	14p11.2-14p11.1	WT-4204

References to the modules:

Pfam: Protein families database of alignments and HMMs

~~(pfam@sanger.ac.uk)~~

PROSITE: The PROSITE database, its status in 1999. Nucleic  
Acids Res. 27: 215-219 ~~(http://www.expasy.ch/sprot/prosite.html)~~



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